

~~#36~~

1636

RAW SEQUENCE LISTING DATE: 07/13/2000
PATENT APPLICATION: US/08/328,673A TIME: 14:06:16

Input Set : A:\169309-2.app
Output Set: N:\CRF3\07132000\H328673A.raw

SEQUENCE LISTING

2

file:///C:/CRF3/Outhold/VsrH328673A.htm

7/13/00

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71      (A) LENGTH: 20 base pairs
72      (B) TYPE: nucleic acid
73      (C) STRANDEDNESS: single
74      (D) TOPOLOGY: linear
W--> 76      (ii) MOLECULE TYPE: DNA
79      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:          20
81 TTCTGGGAAG GGACAGAAGA
84 (2) INFORMATION FOR SEQ ID NO: 3:
86      (i) SEQUENCE CHARACTERISTICS:
87      (A) LENGTH: 25 base pairs
88      (B) TYPE: nucleic acid
89      (C) STRANDEDNESS: single
90      (D) TOPOLOGY: linear
W--> 92      (ii) MOLECULE TYPE: DNA
95      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:          25
97 CGCGCTAGCT CTGCCCAAA GAGCT
100 (2) INFORMATION FOR SEQ ID NO: 4:
102      (i) SEQUENCE CHARACTERISTICS:
103      (A) LENGTH: 39 base pairs
104      (B) TYPE: nucleic acid
105      (C) STRANDEDNESS: single
106      (D) TOPOLOGY: linear
W--> 108      (ii) MOLECULE TYPE: DNA
111      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:          39
113 CGCGGTACCC TCGAGTCTAG ATATTGCCAG TGGTGGAAAG
116 (2) INFORMATION FOR SEQ ID NO: 5:
118      (i) SEQUENCE CHARACTERISTICS:
119      (A) LENGTH: 35 base pairs
120      (B) TYPE: nucleic acid
121      (C) STRANDEDNESS: single
122      (D) TOPOLOGY: linear
W--> 124      (ii) MOLECULE TYPE: DNA
127      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:          35
129 CGTCGGCCG CTGGAGACT TTGAGGATGT CTGTC
132 (2) INFORMATION FOR SEQ ID NO: 6:
134      (i) SEQUENCE CHARACTERISTICS:
135      (A) LENGTH: 33 base pairs
136      (B) TYPE: nucleic acid
137      (C) STRANDEDNESS: single
138      (D) TOPOLOGY: linear
W--> 140      (ii) MOLECULE TYPE: DNA
143      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:          33
145 CGCTCTAGAG AGACCAGTTA GGAAGTTTTC GCA
148 (2) INFORMATION FOR SEQ ID NO: 7:
150      (i) SEQUENCE CHARACTERISTICS:
151      (A) LENGTH: 2995 base pairs
152      (B) TYPE: nucleic acid
153      (C) STRANDEDNESS: single
154      (D) TOPOLOGY: linear

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156	(ii) MOLECULE TYPE: cDNA	
159	(ix) FEATURE:	
160	(A) NAME/KEY: CDS	
161	(B) LOCATION: 139..2925	
162	(D) OTHER INFORMATION: /product= "RB"	
163	/note= "retinoblastoma tumor suppressor"	
166	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
168	TTCCGGTTTT TCTCAGGGAA CCTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG	60
170	GCGGTGCCCG CGCTGCCTCG CCTCCACAGC TCGCTGGCTC	120
172	CCGCCGCGGA AAGGCCTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC	171
173	Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala	
174	1 5 10	
176	ACC GCC GCC GCT GCC GCG GAA CCC CCG GCA CCG CCG CCG CCC	219
177	Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro	
178	15 20 25	
180	CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT	267
181	Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	
182	30 35 40	
184	CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA	315
185	Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala	
186	45 50 55	
188	TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG	363
189	Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	
190	60 65 70 75	
192	TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT	411
193	Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
194	80 85 90	
196	ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA	459
197	Ile Gln Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
198	95 100 105	
200	GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	507
201	Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
202	110 115 120	
204	ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	555
205	Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
206	125 130 135	
208	ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT	603
209	Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
210	140 145 150 155	
212	GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT	651
213	Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
214	160 165 170	
216	ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT	699
217	Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
218	175 180 185	
220	GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	747
221	Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
222	190 195 200	
224	GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	795

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225	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	
226	205					210					215						
228	CTA	TGT	GTC	CTT	GAC	TAT	TTT	ATT	AAA	CTC	TCA	CCT	CCC	ATG	TTG	CTC	843
229	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	
230	220					225				230					235		
232	AAA	GAA	CCA	TAT	AAA	ACA	GCT	GTT	ATA	CCC	ATT	AAT	GGT	TCA	CCT	CGA	
233	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	
234						240				245					250		
236	ACA	CCC	AGG	CGA	GGT	CAG	AAC	AGG	AGT	GCA	CGG	ATA	GCA	AAA	CAA	CTA	939
237	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	
238						255			260			265					
240	GAA	AAT	GAT	ACA	AGA	ATT	ATT	GAA	GTT	CTC	TGT	AAA	GAA	CAT	GAA	TGT	987
241	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	
242						270			275			280					
244	AAT	ATA	GAT	GAG	GTG	AAA	AAT	GTT	TAT	TTC	AAA	AAT	TTT	ATA	CCT	TTT	
245	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	
246						285			290			295					
248	ATG	AAT	TCT	CTT	GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT	CCA	GAG	GTT	GAA	1083
249	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	
250	300					305				310			315				
252	AAT	CTT	TCT	AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	1131
253	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	
254						320			325			330					
256	GAT	GCA	AGA	TTA	TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT	CAG	ACT	GAT	TCT	
257	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	
258						335			340			345					
260	ATA	GAC	AGT	TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	1227
261	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	
262						350			355			360					
264	GAA	GAG	GTG	AAT	GTA	ATT	CTT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	
265	Glu	Glu	Val	Asn	Val	Ile	Ile	Leu	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met
266						365			370			375					
268	AAC	ACT	ATC	CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	1323
269	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	
270	380					385			390			395					
272	CCT	TCA	GAA	AAT	CTG	ATT	TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	1371
273	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	
274						400			405			410					
276	AAA	GAA	AGT	ATA	CTG	AAA	AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	1419
277	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	
278						415			420			425					
280	GAG	AAA	TTT	GCT	AAA	GCT	GTG	GGA	CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	1467
281	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	
282						430			435			440					
284	CAG	CGA	TAC	AAA	CTT	GGA	GTT	CGC	TTG	TAT	TAC	CGA	GTA	ATG	GAA	TCC	1515
285	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	
286						445			450			455					
288	ATG	CTT	AAA	TCA	GAA	GAA	CGA	TTA	TCC	ATT	CAA	AAT	TTT	AGC	AAA		1563
289	Met	Leu	Lys	Ser	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys		

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290	460	465	470	475	
292	CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT				1611
293	Leu Leu Asn Asp Ile Phe His Met Ser Leu Ala Cys Ala Leu				
294	480	485	490		
296	GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT				1659
297	Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp				
298	495	500	505		
300	TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA				1707
301	Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu				
302	510	515	520		
304	AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA				1755
305	Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu				
306	525	530	535		
308	GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT				1803
309	Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His				
310	540	545	550	555	
312	CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT				1851
313	Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp				
314	560	565	570		
316	CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA				1899
317	Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu				
318	575	580	585		
320	TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA				1947
321	Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala				
322	590	595	600		
324	GAT ATG TAT CTT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT				1995
325	Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr				
326	605	610	615		
328	ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC				2043
329	Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala				
330	620	625	630	635	
332	TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT				2091
333	Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr				
334	640	645	650		
336	AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA				2139
337	Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu				
338	655	660	665		
340	CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT				2187
341	Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu				
342	670	675	680		
344	TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT				2235
345	Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His				
346	685	690	695		
348	TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG				2283
349	Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys				
350	700	705	710	715	
352	AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT				
353	Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu				
354	720	725	730		2331

VERIFICATION SUMMARY

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L:29 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:220 C: Keyword misspelled or invalid format, (A) APPLICATION NUMBER:
L:36 M:220 C: Keyword misspelled or invalid format, (B) FILING DATE:
L:39 M:220 C: Keyword misspelled or invalid format, (A) APPLICATION NUMBER:
L:40 M:220 C: Keyword misspelled or invalid format, (B) FILING DATE:
L:60 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1, Value=[DNA]
L:76 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2, Value=[DNA]
L:92 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
L:108 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4, Value=[DNA]
L:124 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[DNA]
L:140 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6, Value=[DNA]